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705					710					715					720
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Ser	Arg	Val	Lys	Gln	Met	Phe	Ala	Ser	Arg	Ala	Cys	Arg	Lys	Ser	Val
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Ala	Leu	Lys	His	His	Thr	Ser	Lys	Leu	Glu	Asp	Phe	Thr	Asp	Leu	Leu

Asn	Leu	Thr	Thr	Tyr	Gly	Phe	Arg	Gly	Glu	Ala	Leu	Ser	Ser	Leu	Cys
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Lys	Thr	Ala	Arg	Gln	Ile	Gly	Thr	Thr	Val	Thr	Val	Arg	Lys	Leu	Phe
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Lys	His	Glu	Asn	Ile	Ser	Thr	Ile	Leu	Ser	Glu	Thr	Pro	Val	Leu	Arg
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Val	Ile	Ser	Lys	Glu	Asp	Met	Thr	Pro	Ser	Glu	Arg	Asp	Ser	Glu	Leu
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Glu	Arg	Asp	Leu	Phe	Ile	Val	Asp	Gln	His	Ala	Ala	Asp	Glu	Lys	Phe
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		595					600					605			

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			100					105					110	Leu
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003221-1036460

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	N	F	K	V	C	V	Q	I	L	R	R	A	T	F	D	V	L	A	L	K
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	H	T	S	K	L	E	D	F	T	D	L	L	N	L	T	T	Y	G	F	R
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361	GGA	GAA	GCC	TTG	AGC	TCT	CTC	TGT	GCA	TTG	GGA	AAT	CTC	ACT	GTG	GAA	ACA	AGA	ACA	AAG
	N	E	P	V	A	T	L	L	T	F	D	H	S	G	L	L	T	A	E	K
421	AAT	GAG	CCA	GTT	GCT	ACG	CTC	TTG	ACG	TTT	GAT	CAT	TCT	GGT	TTG	CTT	ACT	GCT	GAA	AAG
	K	T	A	R	Q	I	G	T	ACT	V	T	V	T	R	K	L	F	S	N	L
481	AAG	ACT	GCT	CGC	CAA	ATT	GGT	ACC	ACT	GTC	ACT	GTT	AGG	AAG	TTG	TTC	TCT	AAT	TTA	CCT
	V	R	S	K	E	F	K	R	N	I	R	K	E	Y	G	K	L	V	S	L
541	GTA	CGA	AGC	AAA	GAG	TTT	AAG	CGG	AAT	ATA	CGC	AAA	GAA	TAT	GGG	AAG	CTT	GTA	TCT	TTA
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601	TTG	AAC	GCA	TAT	CGC	CTT	ATT	GCG	AAA	GGA	GTG	CGG	TTT	GTC	TGC	TCT	AAC	ACG	ACT	GGG
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2281 CCT GAT GAC GAC AAT GTC AAT GAT GAT GAT GAT GAT GAT GCA ACC ATC TCA TTG GCA TGA

Sequence ID 4. *Arabidopsis thaliana* PMS2 homologue (ACCESSION AF069298) cDNA and amino acid sequenc.

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 N R N V I H R I C S G Q V I L D L S S A
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 G E A L S S L C A L G N L T V E T R T K
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 N E P V A T L *
 421 AAT GAG CCA GTT GCT ACG CTC ...

Sequence ID 6. *Arabidopsis thaliana* PMS134 homologue cDNA and amino acid sequences.

1 70

humPMS2 (1) ATGGAGCSAGCTGAGAGCTCGAGACAGAACTGCTAAGGC-----ATCAAACCTATGATCGGAAGT

AtPMS2 (1) ATGCAAGGAGATTCTTCTCCGTC--CGAGACTACTAGCTTCCTTTGATAAGACCTATAACACAAACG

Consensus (1) ATG A GAG T CG T C CT CTA C AT A ACCTAT A G AA

71 140

humPMS2 (65) CAGTCTCATCATTTGCTGTGGGCGGTGGTACTGAGTCTAAGCACTGCGGTAAGGAGTACTAGAAAT

AtPMS2 (71) TCAATTCAGAAATCTGTTCGGGTCAAGTCACTTAGACCTCTCTTGGGCGTCAAGGAGCTTTTCAGAA

Consensus (71) A T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA AA

141 210

humPMS2 (135) CAGTCTCGATGCTGGTGGCAGTATATTATCTAAAGCTTAAGGACTATGGATGGATCTATTGAACTT

AtPMS2 (141) TACTCTCGACCGCGGCCACCGTATAGAGATTAACTCCGAGACTACGGCAAGACTATTTCAGCTC

Consensus (141) AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT

211 280

humPMS2 (205) TCAGACAATGGATGTGGGT-----AGAAGAAG-----AAAACCTCGAAG-----G

AtPMS2 (211) ATTGACAATGGTTGTGGCATTTCCCAACCAATTCAGGTTTGTGTCCAATTCCTCGAAGAACTTTTG

Consensus (211) GACAATGG TGTGG T A AAG AA CT CGAAG G

281 350

humPMS2 (246) CTAAACT---CTCAACATCAACATCTAAGATCTAAGAGTTTGGCGACCTAACTCAGCTGGA-ACT

AtPMS2 (281) AGTTCTTGCACTTAAGCATCATCTTCTAAATTAGCGATTTCAAGATCTTT-CAATTTGACTACTT

Consensus (281) T CT CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT

351 420

humPMS2 (311) TTGGCTTTCCGGGSAAGCTCTCAGCTCACTTTGTGCACTGACCGATGTCACCAITTTCTTCTC--CCAC

AtPMS2 (350) ATGGTTTTCAGGAGAAAGCTTCAGCTCTCTCTGTGCACTGCGAAATCTCACTGTGGAAATTAAGAA

Consensus (351) TGG TTT G GG GAAGC TGAGCTC CT TGTGCA TG G AT TCAC T AC G C A

421 490

humPMS2 (379) GCATCGCGCAAGGTTGGAAGTCTGAGTGAAGTTTGATCAAAATGGGAAATTA-TCAGAAACCCCTAC

AtPMS2 (420) GAATGAGCA--GTTGCTACGTTCTGAGCTTTGATCATTCGTTTGTGTTTACCTGTAAGAAAGACTG

Consensus (421) G AT GC A GTTG AC C TGA GTTGTATCA TGG TTA T C GAAAA

491 560

humPMS2 (448) CCGCCGCCAGAGGACCCACATCTACGCTGCAACAGTTATTTCGACCTACCTGTGGCCATTAAGAA

AtPMS2 (488) CTG-SCGAAATTTGATCCACTCTCACTCTTAGCAAGTTGTTCTCTAATTACCTGTACCAAGCAAGAG

Consensus (491) C C GCC A GG ACCAC GTCA GT G AGTT TT TC A TACCTGT CG AA GA T

561 630

humPMS2 (518) TTCAAAGGAATATTAAGAAGGAGTATGCCAAATGGTCCAGGCTTACATGCATACCTGTATTTTACG

AtPMS2 (557) TTAAAGCGGAATATACGAAAGAAATATGGGAAGCTTTGATCTTTATTGAACGCATATGCGCTATTTCGAA

Consensus (561) TT A GGAATAT AA GA TATG AA T GT T TT A GCATA T ATT C

631 700

humPMS2 (588) AGGCATCCGTCTAAGTTGACCTCTCAGCTTGGACAAAGAAACGACCCCTGTGGTATGCACAGGTCGA

AtPMS2 (627) AGGAGTCCGCTTGTCTGCTCTCAGCACTGGGAA--AACCGAAGTCTGTGTG-----CTCA

Consensus (631) AGG T CG T TGC C AA G TGG AA AA C A AG CTGT GT G GA

701 770

humPMS2 (658) AGCCCAAGCAAAAGGAATATCGGCTCTGTGTTTGGCAGAACAGTTGCAAGCCTCATTCTTTT

AtPMS2 (686) A---CA-CAAA-AGG--G-GG-----G

Consensus (701) A CA CA AA GG A G G G

771 840

humPMS2 (728) TTCAGCTGCCCTAGTACTCCGCTGTGTGAAGAGTACGGTTTGAGCTGTTCCGATGCTCTGCATATCT

AtPMS2 (702) TTCA-----CT-TAAAGA--TAAT-----ATCTAAGASITTT-----TCGCATTAGTA

Consensus (771) TTCA C TA GA T A A AC GTTT TC GCAT A

841 910

humPMS2 (798) TTTTACATCTCAGGTTTCATTTCACAAATGCAACGATGGAGTTGGAAGAGTTCAACAGACAGACAGTT

AtPMS2 (743) CTTTACAAGT-----TACA-GCCTGGTACTGGACGCAATTAGCAGATCGACAGTAA

Consensus (841) TTTACA TC T CA GC TGG TGA G A TT A CAGA GACAGT T

911 980

humPMS2 (868) TTCTTTTATCAACCGCGGCTTGTGACCCAGCAAAGTCTGCAAGCTCTGGAATGAGCTTACCACTG

AtPMS2 (796) TTTCTTTATAAATGCTCGGCGGTAGATATGCCAAAGTCAAGCAAGTTGGTGAATGAGTTATAT-AAAG

Consensus (911) TTCTTTTAT AA G CGGCT GA CAAA GTC GCA T GTGAATGAG T TA A A T

981 1050

humPMS2 (938) ATAA-TCGACACCAATATCCATTTGTTGTTCTTAACTTTCTGTGATTCAGAAATGCGTGCATATCAATG

AtPMS2 (865) ACAAGTCTCGGAAATATCCAGTACCATCTCTGCATTTATGTGCTTGGTGGCATGCTATTTGAATG

Consensus (981) A AA T C A TATCCA TT TTCT A TT TGT T G A TGAT T AATG

1051 1120

humPMS2 (1007) TTACTCCAGATAAAAGGCAAAATTTGCTACAAGAGGAAAGCTTTGTTGGCASTTTAAAGACCTCTTT

AtPMS2 (935) TCAGCCCGATAAAAGAAAGGCTCTTTCTTCTGACGAGCA--CTTCTGTTATCGSTT-----CTTT

Consensus (1051) T AC CC GATAAAAG A T TT T GA GA A CTT GTTT C GTT CTTT

1121 1190

humPMS2 (1077) GATAGGAATGTTTGAATAGTATGTCACAGCTAAATGTCACTCAGCAGCCACTGCTGGAATGTTGAAGGT

AtPMS2 (993) GAG-GGAAGGTCTGA-----A-CGAGATATATCC--H-----CCAGTAATGCCCTTATA---

Consensus (1121) GA GGAA GT TGA A C AG TA AT C T CCA T TG T TT A

1191 1260

humPMS2 (1147) AACTTAATAAAATTCATTCACCGGATTTGGAAGAGCCATGGTAGAAAGCAGGATCAATCCCGTTCA

AtPMS2 (1040) ----TTGTTAATAGTTTCAGGAGATTTGGAGCAACG-----AGATAAG--GCTGGGTTTGTGCT

Consensus (1191) T T AA A G G G G ATT GGA A CC AGA AAG G T A C TC T

1261 1330

humPMS2 (1217) TAAGGACTGCGAAGAAAAAAGACGTGTCATTTTCAGACTGCGAGAGCCCTTTTCTCTTCCTCACAC

AtPMS2 (1097) TTC-----AGAAGAAATCAAA--TCTTTTGTGAGAA-GGATAG-----TTCTGGATGTCACTT

Consensus (1261) T AGAAGAAA AAA TC TT CAGA G GA AG TTCT GTCA 1400

1331 1400

humPMS2 (1287) AACAGAGAACAGCCTCACAGCCCAAGAGCTCCAGACCAAGAGGAGCCCTCTAGGACAGAAAAGGCGT

AtPMS2 (1148) CTAA---AACAGACT---AGGGGAGCTATTGAGAGAGAAAATCCCTCTAAGGAGGTTGAAATTCGA

Consensus (1331) A AACAG CT AG AA T AGAA AA A A CC T GGA AA G

1401 1470

humPMS2 (1357) ATGCTCTCTTCTGCACTTCAGCTGCCATCTCTGACAAAGGCGTCTCTAGACCTCAGAAAACAGGCAGTGA

AtPMS2 (1212) TAATAGTTCGGC---ATGGAGAAGTTTAAGTTTGAGATCAGGCAAG-TGCGACGA-AGAAAGGGGAAG---

Consensus (1401) GT C A AG T T T GA AAGGC T TG GAC AGAAAG GG AG

1471 1540

humPMS2 (1427) GTTCAGTCTCGGACCCAGTGAACCTACGACAGAGCGAGGTGAGAGGACTCGGGGCAAGGAGCAGCAG

AtPMS2 (1277) GTTCT---TCT---CAGT---CCAT---SATGTAACTCCCTGACAG-AGACCTAGCAAAAGTTTGC

Consensus (1471) GTTC T A CAGT CC GA A C A T GA AAG AC C GCA G C

1541 1610

humPMS2 (1497) TTCCGTGGATTCTGAGGCTTTCAGCATCCGAGACACGGGAGTCACTGCAAGCGAGTATGCGGCGAGC

AtPMS2 (1334) CTCAGTTAAATGTGACTG-----AGA-----AAGTACTGATGCA---AGTA-----AAG

Consensus (1541) TC GT A T TGA G AGA AGT ACTG GCA AGTA A

1611 1680

humPMS2 (1567) TCCAGGGGACAGGGGCTCGCAGGACATCTGAGCTCTCAGGAGAAAGCGCTGAACTGACCACTCTT

AtPMS2 (1376) ACTTGAG---CAGCCGCTCT---A-GCTTGCCTGCTCA-----ACTT---TGAATAGTTT

Consensus (1611) C AG CAG GCTC A T TG C TCA CT TGA ACT TT

1681 1750

humPMS2 (1637) TTTCAGATCTGACTGCCATTCAACCCAGCAAGATTCGGATGTAAATTTTCGAGTTTTCCTCAGCCACAG

AtPMS2 (1423) GTTACCATGGG-----AAA-----AAGAAAC-ATGAAAC-CAAGAC-AC

Consensus (1681) TT ATG G AAA AAGA A C ATG AAA C T AGC AC

1751 1820

humPMS2 (1707) TAATCTCGCAACCCCAACACAAAGCGTTTAAAGAAAGAGAAATTCCTTCCAGTTCTGACATTTCGTCAA

AtPMS2 (1461) CTTCCTCTCTG---AAACACCT---CTCCCTCAAAACCA-CACTCT---AGTTAT---CGTGTGAGAC

Consensus (1751) A CTC C AAACAC GT T A AAA A AA TTCT AGTT T C T TG A

1821 1890

humPMS2 (1777) AAGTTAGTAAATACTCAGGACATGTGAGCCTCTCAGGTTGATGTAGCTGTGAAATTAATAAGAGTTG

AtPMS2 (1517) AA---AGCAAAATTGAAGTTCTGCTC-----CTAGCTTC---AGGCTC---CTCGT---AAGGCGC

Consensus (1821) AA AG AAT AG C TG CT AG TT A AG TGT T T G AAG G

1891 1960

humPMS2 (1847) TGCCCTCGACTTCTCTATGASTCTCTAGCTAAACAAATAAAGCAGTTACATCATGAAGCACAGCAAG

AtPMS2 (1568) ATGAACTTGA---TGATATG-G---TCATCTAAAG-----AAGCATGTGACCAAGG---AAAG

Consensus (1891) C CT GA T TATG G T A CT AA G G AG TA CA AAGC AAAG

1961 2030

humPMS2 (1917) TGAAGGGGAACAGAATTACAGGAAGTTAGCGCAAAATTTTCTCTGGAAGAAATCAAGCAAGCCGAAAT

AtPMS2 (1620) AGATTTCTGAAGT-----AGGCAATC---G-----GATTTCTCTGGGACA---CAAGCTCATATCTT

Consensus (1961) GA GAAC AGG A T G GATTT TCCTGGA A CAAGC G A G T

2031 2100

humPMS2 (1987) GAACTAAGAAAGAGATTAAGTAAAGGATGTTTCAGAAATGGAATCA-TGCTCACTTTAACTGGGAT

AtPMS2 (1672) GAA---AGCACTGAGAGA-STA---G-----TCGGCAATTCATCTCTGGT

Consensus (2031) GAA AGA A GAGA A GTA C T GG CA TT AA CT GG T

2101 2170

humPMS2 (2057) TTATATAAGCAAACTGAATGAGGATATCTTCATAGTGGACAGCATGCGACGACGAGAACTATAACTT

AtPMS2 (1712) TCATCATTCGAAATTCGAGCGAGATCTGTTCAATTCGATCAGCATGCGAGTATGAGAAATTCACCTT

Consensus (2101) T AT AT C AAA TG A GAT T TTCAT GTGA CAGCATGC C GA GAGAA T AACTT

2171 2240

humPMS2 (2127) CGAG-ATGCTGCAGCAGCAACCGTGTCTCGGGGCGAGGCTCATAGCA-CCTCAGACTCTCAACTTAA

AtPMS2 (1782) CGAACATTTACCAAGGTCA-ACTGTCTGAGCCAGCA-ACCCTTCTCCAGCTTTGAAGTGGAGCTCT

Consensus (2171) CGA AT GCA CA AC GT CT A GCA A CT A CA CCT GA T A T

2241 2310

humPMS2 (2195) CTGCTGTAACTCAAGCTGTTCTGATAGAAATCTGGCAATATTTAGAAACAAATGGCTTTGATTTCTTAT

AtPMS2 (1850) CTCGCAAGACAGAACTAACTGTCTTAATGACATGGCTATTATCAGGCAAAATGGCTTTCTCTCAGGAG

Consensus (2241) CT C G A GAAG T TG TA A TGGA AT T AG A AATGGCTTT T T G

2311 2380

humPMS2 (2265) CGATGAAATGCTCCAGTCACTGAAAGGGCT--AAACTGATTTCTTTGCCAAGTAGTAAAACTGGACCT

AtPMS2 (1920) GAATCAAGTGTCTC--TCCCGGAAACACTTTAGCTACAGAGCGATTCCTTATAGCAAGATATCACCT

Consensus (2311) AT AA TGCTCC TC C GAAA CT A ACT CC T CC TAG AA AA ACCT

2381 2450

humPMS2 (2333) TCGACCCCAAGACCTCGATGAACTGATCTTCATGCGAGCGAAGCGCTGGGG---TCATGTGCCCG

AtPMS2 (1988) TTGGAGTCCAGATCTTAAAGACCTGATCTCACTCTAGSAGATACCATGGGCAATGTTCCGTTGCTAG

Consensus (2381) T GGA C A GA T A GA CTGATCT A CT G GA A CC TGGGG TC TGC G

2451 2520

humPMS2 (2398) -----CCCTCCGAGTCAAGCAGATGTTTGGCTTCCAGAGC

AtPMS2 (2058) TAGCTACAAAACAGCAAAACAGATTGATTTGTCATGACGAGTCCGTGCAATGCTAGCATCCGAGCA

Consensus (2451) CC TC CGAGTC ATG T GC TCC GAGC

2521 2590

humPMS2 (2434) TGGCGAAGTCTGCTGATGATGCGACTCTCTTAACCAAGCGAGATGAGAAACTGATCACCAGATGG

AtPMS2 (2128) TCGACATCATCTGTGATGATCGAGATCCACTGAGAAACGAAATGAGAGATAGTAGAACACTTGG

Consensus (2521) TGC G TC GTGATGAT GG T C CT A A AA CGA ATG AGAA T T CAC TGG

2591 2660

humPMS2 (2504) GGAGAGTGGACCAACCGCTGGAACTGTCCCATGGAGCCCAACATGACACATCCCAAGCTGGGTGT

AtPMS2 (2198) CAGATCTCAATCTCGTTGGAATTCGCGACACGGACCAACAATGCTCATCTTGTGGAGTTGACAA-

Consensus (2591) GA T GA CC TGGAA TG CC CA GGA G CCAAC ATG G CA T G AC TG

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